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Db      50 GTGTGGAGTAGCTGTAAACACCCCTGTTTATGATAGTATCATATAATTAAC 1

RESULT      5
BGL76206
LOCUS      996 bp      mRNA      EST      06-FEB-2001
DEFINITION      60233535lf2 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4458252 5'
                mRNA sequence.
BGL76206
BGL76206.1  GI:12682909
EST.
                house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 996)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabps.rem@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA library Preparation: Life Technologies, Inc.
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10256 Row: f Column: 13
High quality sequence stop: 668.
                Location/Qualifiers
                1..996
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                /strain="FVB/N"
                /db_xref="taxon:10090"
                /clone="IMAGE:4458252"
                /clone_lib="NCI_CGAP_Mam1"
                /tissue_type="tumor, biopsy sample"
                /dev_stage="3 months, virgin"
                /lab_host="DH108"
                /note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
                Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                Library constructed by Life Technologies. Investigator
                providing samples: Gilbert Smith, NIH"
BASE COUNT      294 a      214 c      243 g      244 t
ORIGIN
Query Match      33.5%; Score 718; DB 174; Length 996;
Best Local Similarity 96.3%; Pred. No. 6.8e-183;
Matches 788; Conservative 0; Mismatches 25; Indels 5; Gaps 5;
QY      865 attgcaactcgaaggaagacaaataatctgcagctattcacaagagcattccaagtccaca 924
Db      1 attggcaattcgaaggaacacaaataatctgcagctattcacaagagcattccaagtccaca 60
QY      925 atggttcattcgaagtagggaaaaaacatggcccttgggtgaatcattcaattttcttc 984
Db      61 ATGGTCATCGAAGTAGGGAAAAAACATGGCCC-TGGGTGAATCATTTCAATTTTCTTC 119
QY      985 gttctgtgtccttttcaataattacggcagaacacgtgggtcattctctttattct 1044
Db      120 GTTTCGTGTCCCTTTTTCATAATTACGGCAGCAACCGTGGGCTATTTCATCTTTTATCT 179
QY      1045 gctcgaagattacgaatgcgaagagctcaagcaggaagcagagcgagtttaaaaggcagat 1104
Db      180 GCTCGAAGATTACGAATCGAAGAGCTCAAGCAGGAGCAGAGCGAGTAAAGGCAGAT 239
QY      1105 gctaaaaagcatttggaagcttcagctgcgcaccttgaacaagaggacaaaggaatt 1164
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QY      1165 gacctgtatggaatagctctctgtgtgacattgaagctataaagccaaatgatattggtg 1224

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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacleb J.M., M.G.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA *The genome sequence of Drosophila melanogaster.*
 RA Science 287:2185-2195(2000).
 RA -!- SIMILARITY: CONTAINS A RING (C3HC4-CLASS) ZINC FINGER.
 RA EMBL: AF003486; AAF47316.1;
 RA FlyBase: FBgn0004919; g01.
 RA InterPro: IPR001841;
 RA InterPro: IPR003015;
 RA Pfam: PF00097; zf-C3HC4; 1.
 RA PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 RA SMART: SM00184; RING; 1.
 RA ZINC-finger.
 RA SEQUENCE 286 AA; 32183 MW; D7A477D8880C682B CRC64;

Query Match 15.7%; Score 357; DB 5; Length 286;
 Best Local Similarity 36.1%; Pred. No. 5.4e-23;
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 b 14 NIAAVITYQNGDLSLTDKGVNVLISIEGRGVRVTISLNRSTVLFVSIFFVLMII 73
 JY 221 TVGVFIYFISAPFLNAPRAQSKORQOLKADAKKAIGKQLRLTKOGKEIGPGDSCAVCI 280
 b 74 SLVWLFYFIYQIRPYMQAQQSKNLGCVTKKAIMKIPTKTGFSO-EKDLSDCAICI 132
 JY 281 ELYKPNLVRILCNHIFHKTCDVDPWLEHRTCPMKCDILKALG... 325
 b 133 EAYKPTDITIRLPCKHBFHKNCDIPWLEHRTCPMKCDILKALG... 192
 JY 326 -----IEVDVGDGVSILQ-VFVSNASNTASPHEDSRSTAS 362
 b 193 TAPTASIEVPVIVVPHGPPQLQPLQASNMSSFAFVFSKRSRPS 242

Sequence
 2
 B

RESULT 7
 ID 076671 PRELIMINARY; PRT: 473 AA.
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 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE H10E21.5 PROTEIN.
 GN H10E21.5
 OS Caenorhabditis elegans
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
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 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RC MEDLINE-94150718; PubMed-7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
 RA Smaildon N., Smith A., Sonnhammer E., Staden R., Sulston J.,

RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston K.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.*
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RC Davidson S., Wohlmann P., Courtney L.,
 RT *The sequence of C. elegans cosmid H10E21.*
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RC Waterston K.,
 RA Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
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 DR InterPro: IPR001841;
 DR InterPro: IPR003015;
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 DR SMART: SM00184; RING; 1.
 DR ZINC-finger.
 SK SEQUENCE 473 AA; 52868 MW; 498647C8B56E0957 CRC64;

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 b 159 SVLFVSIFFIILMW:SLAWLVYVQVFPYAHAKDPLORPLFNARAKAURTPTMTIIPG 218
 QY 266 -DKEIGPGDSCAVCIELYKPNLVRILCNHIFHKTCDVDPWLEHRTCPMKCDILKAL 324
 b 219 MTQELQSD---CAVCLDPYQLQDVIRLLPCKHLYKSCIDPWLLEHRTCPMKCDILKHF 275
 QY 325 GIEVDV-----EDGVSILQVPSVNEASNTASPHEDSRSTASPHGVASVQ 370
 b 276 GYWNDRINDIOPTNSRGIAADFTIRLEGEQHOAPSADVISPEANSDTSQSGFSFN 335
 QY 371 ADPPLEEAQAQSANML--OLYNHEANS 396
 b 336 SEHHHSFSGYGTSTVPPPLVNASNA 363

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 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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 GN RZF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Lomax M.I., Warner S.J., Bersirri C.G., Gong T.-W.L.;
 RL Prim. Sens. Neuron 0:0-0(1998).
 CC -!- SIMILARITY: CONTAINS A RING (C3HC4-CLASS) ZINC FINGER.
 DR EMBL: AF037205; AAC03770.1;
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 DR InterPro: IPR003137;
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF02225; PA; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
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